

SEQUENCE



#6

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lindler, Luther E
Warren, Richard
VanDeBerg, Lillian
Rubin, Fran
- (ii) TITLE OF INVENTION: Protein From Brucella Species
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Associates
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: Virginia
 - (E) COUNTRY: United States
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/785,689
 - (B) FILING DATE: 20-FEB-2001
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna
 - (B) REGISTRATION NUMBER: 32,535
 - (C) REFERENCE/DOCKET NUMBER: lindler
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 425-8405
 - (B) TELEFAX: (703) 425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brucella

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCTGACAT AACCCGCTTT GTCCAAATTT TTTCAACTTT TCCTGTAGGA GATTTTATGA	60
ACACTCGTGC TAGCAATTTT CTCGCAGCCT CATTTTCCAC AATCATGCTC GTCGGCGCTT	120
TCAGCCTGCC CGCTTTCGCA CAGGAGAATC AGATGACGAC GCAGCCCGCG CGCATCGCCG	180
TCACCGGGGA AGGCATGATG ACGGCCTCGC CCGATATGGC CATTCTCAAT CTCTCGGTGC	240
TACGCCAGGC AAAGACCGCG CGCGAAGCCA TGACCGCGAA TAATGAAGCC ATGACAAAAG	300
TGCTCGATGC CATGAAGAAG GCCGGCATCG AAGATCGCGA TCTCCAGACA GCGGGCATCA	360
ATATCCAGCC GATTTATGTC TATCCTGACG ACAAGAACAA CCTGAAAGAG CCTACCATCA	420
CCGGCTATTC TGTATCCACC AGTCTCACGG TTCGCGTGCG CGAACTGGCC AATGTTGGAA	480
AAATTTTGGGA TGAATCCGTC ACGCTCGGTG TTAATCAGGG CGGTGATTTG AACCTGGTCA	540
ATGATAATCC CTCCGCCGTG ATCAACGAGG CGCGCAAGCG CGCAGTGGCC AATGCCATTG	600
CCAAGGCGAA GACGCTTGCC GACGCTGCAG GCGTGGGGCT TGGCCGTGTG GTGGAAATCA	660
GTGAACTGAG CCGCCCGCCC ATGCCGATGC CAATTGCGCG CGGACAGTTC AGAACCATGC	720
TAGCAGCCGC ACCGGACAAT TCCGTGCCGA TTGCCGCAGG CGAAAACAGC TATAACGTAT	780
CGGTCAATGT CGTTTTTGAA ATCAAGTAAA TAGCTGGGGT ATGACGCCCT TTGCCACCTG	840
ATACAAAACG CCGGCCTGGT TTCACAGGCC GGTTTTTTTG ATTAGAGCGC GTTTCGATCT	900
GATTGAATCC GATCGGCGCT CTAATCCTTT GTTTTGACGC GCATCTTTTC CGAAAACCGT	960
TTCACACTTT TCGGGATGCG GTCTAGCGGA TGATCGGGCA ACCGCGCGTA TCGGCAAATG	1020
TCACG	1025

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brucella

(B) STRAIN: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Thr Arg Ala Ser Asn Phe Leu Ala Ala Ser Phe Ser Thr Ile
1 5 10 15

Met Leu Val Gly Ala Phe Ser Leu Pro Ala Phe Ala Gln Glu Asn Gln
20 25 30

Met Thr Thr Gln Pro Ala Arg Ile Ala Val Thr Gly Glu Gly Met Met
35 40 45

Thr Ala Ser Pro Asp Met Ala Ile Leu Asn Leu Ser Val Leu Arg Gln
50 55 60

Ala Lys Thr Ala Arg Glu Ala Met Thr Ala Asn Asn Glu Ala Met Thr
65 70 75 80

Lys Val Leu Asp Ala Met Lys Lys Ala Gly Ile Glu Asp Arg Asp Leu
85 90 95

Gln Thr Gly Gly Ile Asn Ile Gln Pro Ile Tyr Val Tyr Pro Asp Asp
100 105 110

Lys Asn Asn Leu Lys Glu Pro Thr Ile Thr Gly Tyr Ser Val Ser Thr
115 120 125

Ser Leu Thr Val Arg Val Arg Glu Leu Ala Asn Val Gly Lys Ile Leu
130 135 140

Asp Glu Ser Val Thr Leu Gly Val Asn Gln Gly Gly Asp Leu Asn Leu
145 150 155 160

Val Asn Asp Asn Pro Ser Ala Val Ile Asn Glu Ala Arg Lys Arg Ala
165 170 175

Val Ala Asn Ala Ile Ala Lys Ala Lys Thr Leu Ala Asp Ala Ala Gly
180 185 190

Val Gly Leu Gly Arg Val Val Glu Ile Ser Glu Leu Ser Arg Pro Pro
195 200 205

Met Pro Met Pro Ile Ala Arg Gly Gln Phe Arg Thr Met Leu Ala Ala
210 215 220

Ala Pro Asp Asn Ser Val Pro Ile Ala Ala Gly Glu Asn Ser Tyr Asn
225 230 235 240

Val Ser Val Asn Val Val Phe Glu Ile Lys
245 250